

Amendments to the Specification:

Please replace the paragraph beginning at page 5, line 8, with the following amended paragraph:

As used herein, "KIM-1 cytoplasmic domain" means amino acids 312-334 of ~~SEQ ID NO:1~~ SEQ ID NO:2, or 312-359 of ~~SEQ ID NO:2~~ SEQ ID NO:1.

Please replace the paragraph beginning at page 5, line 22, with the following amended paragraph:

**FIG. 1** (prior art) is a schematic representation of two naturally-occurring splice variants of the human KIM-1 polypeptide (top variant is SEQ ID NO:2; bottom variant is SEQ ID NO:1). The two amino acid sequences are identical through residue 323. The signal sequence (residues 1-20) is indicated by an underline. The transmembrane domain (residues 290-311) is indicated by a double underline.

Please replace the paragraph beginning at page 8, line 5, with the following amended paragraph:

The native human KIM-1 gene encodes a polypeptide (FIG. 1) containing 334 amino acids or 359 amino acids (~~SEQ ID NO:1~~ SEQ ID NOs:2 or 1, respectively), depending on splice variation, which is at least partially tissue-dependent. Both sequences include: a signal sequence, an Ig domain, a mucin domain, a transmembrane domain, and a cytoplasmic domain.

Please replace the paragraph beginning at page **17**, line **12**, with the following amended paragraph:

Other derivatives of KIM-1 polypeptides include covalent or aggregate conjugates of modified KIM-1 or its fragments with other proteins or polypeptides, such as by synthesis in recombinant culture as additional N-termini, or C termini. For example, the conjugated peptide may be a signal (or leader) polypeptide sequence at the N-terminal region of the protein which co-translationally or post-translationally directs transfer of the protein from its site of synthesis to its site of function inside or outside of the cell membrane or wall (e.g., the yeast alpha-factor leader). KIM-1 polypeptides can be fused to heterologous peptides to facilitate purification or identification of the KIM-1 moiety (e.g., histidine/KIM-1 fusions). The KIM-1 moiety also can be linked to the peptide Asp-Tyr-Lys-Asp-Asp-Asp-Lys (DYKDDDDK) (~~SEQ ID NO:~~ SEQ ID NO:6) (Hopp et al., 1988, *Biotechnology* 6:1204). This sequence is highly antigenic and provides an epitope reversibly bound by a specific monoclonal antibody. Consequently, it facilitates assay and purification of the expressed recombinant protein. This sequence is specifically cleaved by bovine mucosal enterokinase at the residue immediately following the Asp-Lys pairing.

Please replace the paragraph beginning at page **30**, line **24**, with the following amended paragraph:

The extracellular domain (residues 1-290) of human KIM-1 was fused to the Fc portion of human IgG1 (hinge, CH2, CH3) and cloned into pEAG347, a Biogen mammalian expression plasmid. The plasmid contained a tandem promotor for constitutive expression and the dihydrofolate reductase gene for methotrexate selection of stably expressing cell lines. The amino acid sequence of the encoded fusion polypeptide was as follows:

1            10            20            30            40            50            60  
MHPQVVILSLILHLADSVAGSVKVGGEAGPSVTLPCHYSGAVTSMCWNRGSCSLFTCQNG

70 80 90 100 110 120  
IVWINGTHVTRYKDDTRYKLLGDLRRDVS LTIENTAVSDSGVYCCRVHRGWFNDMKITV

130 140 150 160 170 180  
SLEIVPPKVTITPIVTIVPTVTTVRTSTTVPTTTTVPITTM SIPTTTTVPTMTIVS

190 200 210 220 230 240  
TTTSVPTTTSIPTTTSVPVTTTVSTFVPPMPLPRQNHPEVATSPSSPQPAETHPTTLQGA

250 260 270 280 290 300  
IRREPTSSPLYSYTTDGN DTVTESSDGLWNNNQTLFLEHSLLTANTTKGVDKTHTCPPC

310 320 330 340 350 360  
PAPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT

370 380 390 400 410 420  
KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY

430 440 450 460 470 480  
TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSK

490 500 510 518  
LTVDKSRWQQGNV FSCSV MHEALHNHYTQKSLSLSPGK (SEQ ID NO:3)

Please replace the paragraph beginning at page 31, line 30, with the following amended paragraph:

DNA encoding residues 1-129 of human KIM-1 fused to the Fc portion of human IgG1 (hinge, CH2, CH3) was cloned into pEAG347, a Biogen mammalian expression plasmid containing a tandem promoter for constitutive expression and the dihydrofolate reductase gene for methotrexate selection of stably expressing cell lines. The amino acid sequence of the encoded fusion polypeptide was as follows:

10 20 30 40 50 60  
MHPQVVILSLILHLADSVAGSVKVGGEAGPSVTLPCHYSGAVTSMCWNRGSCSLFTCQNG  
70 80 90 100 110 120  
IVWTNGTHVTYRKDTRYKLLGDLRRDVS LTIENTAVSDSGVYCCRVEHRGWFNDMKITV  
130 140 150 160 170 180  
SLEIVPPKVVDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHED  
190 200 210 220 230 240  
PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA  
250 260 270 280 290 300  
PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN  
310 320 330 340 350  
YKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID  
NO:4)

Please replace the paragraph beginning at page 33, line 2, with the following amended paragraph:

The extracellular domain (residues 1-290) of human KIM-1 was fused to a short C-terminal peptide [VEHHHHHH; SEQ ID NO:5] including a repeat of 6 histidine residues and cloned into pCA125, a BIOGEN mammalian expression plasmid containing a CMV promoter for transient constitutive expression in mammalian cells. The amino acid sequence of the encoded fusion polypeptide was as follows:

10 20 30 40 50 60  
MHPQVVILSLILHLADSVAGSVKVGGEAGPSVTLPCHYSGAVTSMCWNRGSCSLFTCQNG  
70 80 90 100 110 120  
IVWTNGTHVTYRKDTRYKLLGDLRRDVS LTIENTAVSDSGVYCCRVEHRGWFNDMKITV

130 140 150 160 170 180  
SLEIVPKVTTTTPIVTTVPTVTTVRTSTTVPTTTTVPTTTTVPTTMSIPTTTTVPTTMTVS  
190 200 210 220 230 240  
TTTSVPTTTSIPTTTSVPVTTTVSTFVPPMPLPRQNHEPVATSPSSPQPAETHPTTLQGA  
250 260 270 280 290  
IRREPTSSPLYSTTDGNDTVTESSDGLWNNNQTLFLEHSLLTANTTKGVEHHHHHH (SEQ ID NO:7)

Please replace the paragraph beginning at page 33, line 25, with the following amended paragraph:

A PCR-amplified ectodomain of murine kim-1 flanked by NotI and SalI sites was fused with human IgG1Fc (isolated from EAG409 as a SalI-NotI fragment) and cloned into Ebna 293 cell expression vector CH269 (construct PEM073-6) and CHO cell expression vector pV90 (construct PEM078-1). The SalI site is at the junction between kim1 and Fc. The resulting nucleotide sequence of the ORF for the fusion protein was as follows (SalI site in upper case):

atgaatcagattcaagctctcattcaggcctcatactgcttctccaggcactgtggattcttatgtggaagtaaaggg  
ggtagtgggtcacctgtcacactccatgtactactcaacatatcgtggaatcacacgacatgtggggccgagggc  
aatgccattctctgctgtcaaaatacacttattggaccaatggacatcgtgtcacctacagaagagcagtcggtac  
aactaaaggggcataattcagaaggagatgtgtcctgacgatagagaactctgtgagagtgacagtggtctgtattg  
ttgtcagtgaggagattcctggatggttaaatgatcagaaagtacacctttcattgcaagtaaacaggagattccacac  
gtcctccaacaagaccacaactacaaggccacagctacaggaagaccacgactatttcacaagatccacacatgta  
ccaacatcaatcagagtctctacctccactctccaacatctacacacacatggactcacaaaccagaaccactacatt  
ttgtcccatgagacaacagctgaggtgacaggaatccatcccatcctacagactggaatggcactgcgacatcct  
caggagatacctggagtaatacactgaagcaatccctccagggaagccgcagaaaaacacctactaagggcGTTCGACaaaactcac  
acatgccaccgtgccagcactgaactcctgggggaccgtcagttctctctcccccaaaacccaagga  
cacctcatgatctccggacccctgaggtcacatgcgtggtgggacgtgagccacgaagacctgaggtcaagttca

actggtacgtggacggcgtggaggtgcataatccaagacaagccgaggagagcagtacaacagcacgtaccgtgtg  
gtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggagfacaaagtccaaggtccaacaaagccctccc  
agccccatcgagaaaaccatctccaaagccaaggcagccccgagaaccacaggtgtacacctcccccatccggg  
atgagctgaccaagaaccaggtcagcctgacgtcctgggtcaaaggcttctatcccagcgacatcgccgtggagtgaggag  
agcaatgggcagccggagacaactacaagaccacgctcccgtgttgactccgacggctccttctctctacagcaa  
gtcaccgtggacaagagcaggtggcagcaggggaacgtcttctatgctccgtgatgcatgaggctctgcacaaccact  
acacgcagaagagcctctcctgtctctccgggaaatga (SEQ ID NO:8)

Please replace the paragraph beginning at page **34**, line **18**, with the following amended paragraph:

The translated sequence of mukim-1 ectodomain-human Fc was as follows. Two junction amino acids contributed by the SalI site are indicated in bold:

MNQIQVFISGLILLPGTVDSYVEVKGVVGHVPTLPCTYSTYRGITTCWGRGQCPSSAC  
QNTLIWTNGHRVITYQSSRYNLKGHISEGDVSLTIENSVESDGLYCCRVEIPGWFNQDQ  
KVTFSLQVKPEIPTRPPTTRPTATGRPTTISTRSTHVPTTSIRVSTSTPPTSTHTWTHKP  
EPTTFCPHETTAEVTGIPSHTPTDWNGTATSSGDTWSNHTEAIPPGKPQKNPTKG**VDK**TH  
TCPPCPAPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE  
VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKISKAKG  
QPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDS  
DGSFFLYSKLTVDKSRWQQGNVFCSTMHEALHNHYTQKSLSLSPGK (SEQ ID NO:9)